

FIGURE 1

CGGACGCGTGGGACCCATACTTGCTGGTCTGATCCATGCACAAGGCGGGGCTGCTAGGCCTC
TGTGCCCGGGCTTGGAATTGCGTGCGGATGGCCAGCTCCGGGATGACCCGCCGGGACCCGCT
CGCAAATAAGGTGGCCCTGGTAACGGCCTCCACCGACGGGATCGGCTTCGCCATCGCCCGGC
GTTTGGCCACGACGCGGGCCCATGTGGTTCGTGAGCAGCCGGAAGCAGAGAATGTGGACCAG
GCGGTGGCCACGCTGCAGGGGAGGGGCTGAGCGTGACGGGCACCGTGTGCCATGTGGGGAA
GGCGGAGGACCGGGAGCGGTGGTGGCCACGGCTGTGAAGCTTCATGGAGGTATCGATATCC
TAGTCTCCAATGCTGCTGTCAACCTTTCTTTGGAAGCATAATGGATGTCACTGAGGAGGTG
TGGGACAAGACTCTGGACATTAATGTGAAGCCCCAGCCCTGATGACAAAGGCAGTGGTGCC
AGAAATGGAGAAACGAGGAGGCGGCTCAGTGGTGATCGTGTCTTCCATAGCAGCCTTCAGTC
CATCTCCTGGCTTCAGTCCTTACAATGTCAGTAAAAACAGCCTTGCTGGGCTGACCAAGACC
CTGGCCATAGAGCTGGCCCCAAGGAACATTAGGGTGAAGTGCCTAGCACCTGGACTTATCAA
GACTAGCTTCAGCAGGATGCTCTGGATGGACAAGGAAAAAGAGGAAAGCATGAAAGAAACCC
TGCGGATAAGAAGGTTAGGCGAGCCAGAGGATTGTGCTGGCATCGTGTCTTTCTGTGCTCT
GAAGATGCCAGTACATCACTGCGGAAACAGTGGTGGTGGTGGAGGAACCCCGTCCCGCCT
CTGAGGACCGGAGACAGCCACAGGCCAGAGTTGGGCTCTAGCTCCTGGTGCTGTTCTGTC
ATTCACCCACTGGCCTTTCCACCTCTGCTCACCTTACTGTTTACCTCATCAAATCAGTTCT
GCCCTGTGAAAAGATCCAGCCTTCCCTGCCGTCAAGGTGGCGCTTACTCGGGATTCCTGCT
GTTGTTGTGGCCTTGGGTAAAGGCCTCCCCTGAGAACACAGGACAGGCCTGCTGACAAGGCT
GAGTCTACCTTGGAAGACCAAGATATTTTTCTTGGGCCACTGGTGAATCTGAGGGGTGA
TGGGAGAGAAGGAACCTGGAGTGAAGGAGCAGAGTTGCAAATTAACAGCTTGCAAATGAGG
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FIGURE 2

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35672
><subunit 1 of 1, 278 aa, 1 stop
><MW: 29537, pI: 8.97, NX(S/T): 1
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SRKQQNVDDQAVATLQGEGLSVTGTVCHVGKAEDRERLVATAVKLHGIDILVSNAAVNPFFG
SIMDVTEEVWDKTLTDINVKAPALMTKAVVPEMEKRGGSVVIVSSIAAFSPSPGFSYPNVSK
TALLGLTKTLAIELAPRNIRVNCLAPGLIKTSFSRMLWMDKEKEESMKETLRIRRLGEPEDC
AGIVSFLCEDASYITGETVVVGGGTPSRL
```

Important features of the protein:

Signal peptide:

amino acids 1-15

N-glycosylation site.

amino acids 183-186

N-myristoylation sites.

amino acids 43-48, 80-85, 191-196, 213-218, 272-277

Microbodies C-terminal targeting signal.

amino acids 276-278

FIGURE 3

GCGCCCTGAGCTCCGCCCTCCGGGCCGATAGCGGCATCGAGAGCGCCTCCGTGAGGACCAGGCGGGG
 CAGGGGGCCGGCGGGCGAAAGGAGGATGAGGGGGCGCAGCAGCTGTGACCCTGCAGAAACAGGTGGC
 GCGGCTGGAGGAGGAGAAACCGAGACTTTCTGGCTGCGCTGGAGGACGCGCATGAGGAGCAGTACAACTGC
 AGAGCGACCCGGCTGCGTGGAGCAGCAGGAGGAGATGGTGGAACTGCGGCTGCGGTTAGAGCTGGTGCGG
 CCAGGCTGCGGGGGCTCGGGCTCTGAATGGCCTGCTCCCGGGTCTTTGTGCGCTCGACCTCATAC
 AGCCCCCTTGGGGGGTGCCACGCCCATGTGCTGGGCATGGTGCCGCTGCTGCCCTCCCTGGAGATG
 AAGTTGGCTCTGAGCAGAGGGGAGAGCAGGTGACAAATGGCAGGGAGGCTGGAGCTGAGTTGCTGACT
 GAGGTGAACAGGCTGGGAAGTGGCTCTTCAGCTGCTTCAGAGGAGGAAGAGGAGGAGGAGGAGCCGCC
 CAGGCGGACCTTACACTGCGCAGAAATAGGATCAGCAACTGCAGTACAGAGGGCGGGGGCAGCCAG
 CGAGTCTGCGCAGAGAGGAAGGCCCAGAGCTTTGCTTGAAGGAGTTGGATGCAGCCATTCACAGGCTCC
 AGAGCAGTTGGTGGGAGCAAGGCCGAGTTTCAGGCCCGCAGGTCCCCCTGCCACAGCCTCAGAGTG
 GCGGCTGGCCAGGCCCCAGCAGAAGATCCGGGAGCTGGCTATCAACATCCGCATGAAGGAGGAGCTTA
 TTGGCGAGCTGGTCCGCACAGGAAGGCAGCTCAGGCCCTGAACGCCAGCACAGCCAGCGTATCCGG
 GAGCTGGAGCAGGAGGCAGAGCAGGTGCGGGCCGAGCTGAGTGAAGGCCAGAGGCAGCTGCGGGAGCT
 CGAGGCGCAGGAGCTCCAGGATGCTGGCGAGCGGTCTCGGCTCAGGAGTTCCGCAGGAGGGGTGCGTGT
 CGGCCCAGAGCCAGGTGCGAGTGTGCTGAAGGAGAAGAAGCAGGCTACGAGGCGGTCTGGTGTCACTGTG
 GCCCAGAGTGAGAAAGCGACTGCAGGAGCTCGAGCGGAAAGTGCAGCTCATGCCGAGCAGCAGGGACA
 GCTGCAGAGCGGGCTTCGCGAGGAGACGGAGCAGAAGCGCGCCTGGAGGCAGAAATGAGCAAGCGGC
 AGCACCGGTCAAGGAGCTGGAGCTGAAGCATGAGCAACAGCAGAAGATCCTGAAGATTAAGACGGAA
 GAGATCGCGGCTTTCAGAGGAAGAGGCGCAGTGGCAGCAACGGCTCTGTGGTGCAGCTTGAACAGCA
 GCAGAAGATTGAGGAGCAGAAAGTGGCTGGACCAGGAGATGAGAAAGGTGCTACAGAGCGCGGGG
 CGCTGGAGGAGCTGGGGGAGGAGCTCCAAAGCGGGAGGCCATCTGGCCAAAGAGGAGGCCCTCATG
 CAGGAGAAGCAGGGGCTGGAGAGCAAGCGCTGAGATCCAGCCAGGCCCTCAACAGGAGCATCGTGGC
 AGTGTCCAGCCGGCTGGAGCACCTGGAGAAGGAGCTGTCCGAGAAGAGCGGGCAGTCCGGCAGGACA
 GCGCCAGAGCCAGCAGCAGATCCGCGGGGAGATCGACAGCTGCGCCAGGAGAAGGACTCGTGTCTC
 AAGCAGCGCTGGAGATCGACGGCAAGCTGAGCGAGGGAGTCTGTGTCCCCGAGGAGGAGCGGAG
 GCTGTTCCAGTTGGATGAGGCCATCGAGGCCCTGGATGCTGCCATTGAGTATAAGAATGAGGCCATCA
 CATGCCGCCAGCGGGTGCTTCGGGCCCTCAGCCTCGTTGTCTGCCAGTGCAGATGAACCTCATGGCC
 AAGCTCAGCTACCTCTCATCTTCAGAGACCAGAGCCCTCCTCTGCAAGTATTTTGACAAAGTGGTGAC
 GCTCCGAGAGGAGCAGCACAGCAGCAGATTTGCTTCTCGGAATCGGAGATGCAGCTGGAGGAGCAGC
 AGAGGCTGTGTACTGGCTGGAGGTGGCCCTGGAGCGGCAGCGCTGGAGATGGACCGCCAGCTGACC
 TCGCAGCAGAAGGAGCACGAGCAGAAATGCAGCTGCTCTCGCAGCAGAGTCGAGACCACCTCGGTGA
 AGGGTTAGCAGACAGCAGGAGGAGCAGTATGAGGCCGGATTCAAGCTCTGGAGAAGGAACCTGGGCGGTT
 ACATGTGGATAAACACGGAACCTGAACAGAGCTCGGCGGTGTGAACGCTGTAGGCCACAGCAGGGGT
 GGGGAGAAGAGGAGCTGTGCTCGGAGGGCAGACAGGCTCCTGGAAATGAAGATGAGCTCCACTGGC
 ACCCGAGCTTCTCTGGCTGTCCCCCTCACTGAGGGGGCCCCCGCACCCGGGAGGAGACGCGGGACT
 TGGTCCACGCTCCGTTACCTTTGACCTGGAACGCTCGAGCCTGTGTGGTGAAGAGAGGGGTCCCC
 GAGGAACCTGAGTCAGGCGGAGCGGCTGAGCCCTGGTGGGGCGGGTCTTCTGTGGGTGAGCGAGG
 CTTGCCCTGGAACCTTTGGGCCCTTTGTCCAAGCCCCGCGGGAAGTGCACGAGGCCAGCCCGGGATGA
 TTGATGTCCGGAACAAACCCCTGTAAAGCCCTCGGGGCAGACCTGCCCTGGAGGGAGACTCGAGCCT
 CTGTAAGGGGCAGCTGCCCTGTTTGGCTTCTGTGAAGGCGAGTCCCTTACCGCACACCTCAATTCAGG
 CCTCATCTGTACCTCTACTGGGATCAACAAATTTGGGCCATGGCCCAAAAGAACTGGACCTCATTT
 AACAAAAATATGCAAAATCCCACCATTACTTCCATGAAGCTGTGGTACCCAAATTCGCCGCTGTGT
 TCTTGTCTGAATCTCAGGACAATTTGGTTTCAGGCGTAATGAGATGCTGTGTAGTTCAAGGGTTTG
 GCCAAGAATCATCAGAAAGGGTCGGTGGCAACAGGTTGTGGTTTAAATGGTCTTATGTATAGGG
 GAAACTGGGAGACTTTAGGATCTTAAAAACCATTTAATAAAAAAAATCTTTGAAGGGAG

FIGURE 4

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA47465

<subunit 1 of 1, 830 aa, 1 stop

<MW: 95029, pI: 8.26, NX(S/T): 2

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LGMVPPACLPQDEVGSEQRGEQVTNGREAGAEALLTEVNRLGSGSSAASEEEEEEEPPRRTL
HLRRNRISNCSQRAGARPGSLPERKGPCLCEELDAAIPGSRAVGGSKARVQARQVPPATAS
EWRLAQAOQKIRELAINIRMKEELIGELVRTGKAAQALNRQHSQRIRELEQEAQVRAELSE
GQRQLRELEGKELQDAGERSRLQEFRRRVAAAQSQVQLKEKKQATERLVSLSAQSEKRLQE
LERNVQLMRQQCGQLQRRRLREETEQRRLLEAEMSKRQHRVKELELKHEQQQKILKIKTEEIA
AFQRKRSGSNGSVVSLEQQQKIEEQKKWLDQEMEKVLQRRALEELGEELHKREAILAKKE
ALMQEKTGLESKRLRSSQALNEDIVRVSSRLEHLEKELSEKSGQLRQGSASQSQQIRGEIDS
LRQEKDSSLKQRLIEDGKLRQGSLLSPFEEERTLFLQDEAIEALDAAIEYKNEAITCRQRVLR
ASASLLSQCEMNLMAKLSYLSSETRALLCKYFDKVVTLREEHQHQQIAFSELMQLEBQQR
LVYWLEVALERQRLQEMDRQLTLQQKEHEQNMQLLLQQSRDHLGEGGLADSRQYEARIQALEK
ELGRYMWINQELKQKLGGVNAVGHSGGGEKRLCSEGRQAPGNEDELHLAPELLWLSPLTEG
APRTREETRDVLVHAPLPLTWKRSSLGEGEQGSPEELRQREAAEPLVGRVLPVGEAGLPWNFG
PLSKPRELRRASPGMIDVRKNPL

Important features:

Leucine zipper pattern.

amino acids 557-579, 794-815

N-glycosylation sites.

amino acids 133-136, 383-386

Kinesin related protein Kif-4 Coiled-coil domain:

amino acids 231-672

FIGURE 5

ATTCCTCTAGAGCATCTTTGGAAGCATGAGGCCACGATGCTGCATCTTGGCTCTTGTCTGCT
GGATAACAGTCTTCCTCCTCCAGTGTTCAAAAGGAACACAGACGCTCCTGTGGCTCAGGA
CTGTGGCTGTGCCAGCCGACACCCAGGTGTGGGAACAAGATCTACAACCCCTTCAGAGCAGTG
CTGTTATGATGATGCCATCTTATCCTTAAAGGAGACCCGCCGCTGTGGCTCCACCTGCACCT
TCTGGCCCTGCTTTGAGCTCTGCTGTCCCGAGTCTTTTGGCCCCCAGCAGAAGTTTCTTGTG
AAGTTGAGGGTTCTGGGTATGAAGTCTCAGTGTCACTTATCTCCCATCTCCCGAGCTGTAC
CAGGAACAGGAGGCACGTCTGTACCCATAAAAAACCCAGGCTCCACTGGCAGACGGCAGAC
AAGGGGAGAAGAGACGAAGCAGCTGGACATCGGAGACTACAGTTGAACTTCGGAGAGAAGCA
ACTTGACTTCAGAGGGATGGCTCAATGACATAGCTTTGGAGAGGAGCCAGCTGGGGATGGC
CAGACTTCAGGGGAAGAATGCCTTCCTGCTTCATCCCCCTTCCAGCTCCCCCTTCCCGCTGAG
AGCCACTTTCATCGGCAATAAAATCCCCACATTTACCATCT

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA57700
><subunit 1 of 1, 125 aa, 1 stop
><MW: 14198, pI: 9.01, NX(S/T): 1
MRPRCCILALVCWITVFLQCSKGTDDAPVGSGLWLCQPTPRCGNKIYNPSEQCCYDDAILS
LKETRRCGSTCTFWPCFELCCPESFGPQKFVLVGLRVLGKMSQCHLSPIRSCTRNRRHVLYP
```

Important features:

Signal sequence

amino acids 1-21

N-myristoylation sites.

amino acids 33-39, 70-76

FIGURE 7

CCCACGCGTCCGCCCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCT
TTTCCCTCCGACGCGCCACGGGTGCCCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCG
AACCCCTCCGCGGAGAGGAGCGAGGCGCGCCAGGTTGGCCCCGGGGCGCGCTTGGTCTCG
GAGAAGCGGGGACGAGGCCGGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTT
GGGGCCGCGACTACCGGCAGCTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCG
GTGTGCGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGG
TCGCGGCGCCGGCCAGGATGGGCGCTGGCAACCCGGGCCCCGCGCCCGCGCTGTACCCCTG
CGCCCGCTGCGAGCCCGCGCTCCGGCCCCGCGCCCTGCGCTCATGGACGGCGGCTCCCGGCTG
GCGGCGGCGCGCCCCCGGGTGTGAATGCGACTCGCCCCTCGGCCGCGCTCCCCGCGCGCC
GCCCGCCGGGACGTGGTAGGGGATGCCAGCTCCACTGCGATGCGAGTTGGCGCGCTCTCCA
GTTCCCTCCTGGTCACCTGCTGCTGATGGTGGCTCTGTGCAGTCCGAGCATCCCGCTGGAG
AAGTGGCCACGGCACCAGAGCAGCCGGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGG
CCCGGGGCGGGTGAACGAGCTCGGGCGCCCGCGAGGGACGAGGGCGGACGCGCCGGGACT
GGAAGAGCAAGAGCGGCCGTGGGCTCGCCGGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCC
TGGGTCTCCAGGGCGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACAC
CCCGCAGGCGGAAGCCCTGGCCGCGAGCCGCCAGGACGCGATTGGCCCGGAACCTCGCGCCCA
CGCCCGAGCCACCCGAGGAGTACGTGTACCCGGACTACCGTGCGCAAGGGCTGCGTGGACGAG
AGCGGCTTCGTGTACGCGATCGGGGAGAAGTTGCGCGCGGGGCCCTCGGCCCTGCCCTGCCT
GTGCACCGAGGAGGGGCCGCTGTGCGCGCAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCA
TCCACGTGACACGAGCCAGTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTC
CGGGGCAAGACCTATCAGACTTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTGCTG
TGAAGCCAAACGGTGAGGTGCTATGCACAGTGTGAGCGTGTCCCAGACGGAGTGTGTGGACC
CTGTGTACGAGCCTGATCAGTGCTGTCCCATGTGCAAAAATGGTCCAAACTGCTTTTGAGAA
ACCGCGTGATCCCTGCTGCGAGAGAAGTGAAGACTGACGAGTGACCATATGCCACTGTAC
TTATGAGGAAGGCACATGGAGAATCGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGC
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AAAACATCAACAAGAACTTTGGGCATAAAATCCTTCTCTAAATAAATGTGCTATTTTCACAG
TAAGTACACAAAAGTACACTATTATATATCAAATGTATTTCTATAATCCCTCCATTAGAGAG
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AAAAAAAAAAAAAAAAAAAA

FIGURE 8

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><subunit 1 of 1, 325 aa, 1 stop
><MW: 35296, pI: 5.37, NX(S/T): 0
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AAAQDAIGPELAPTEPPPEEYVYPDYRGKGCVDSEGFVYAIGKFAPGPSACPLCTEEGPL
CAQPECPRLHPRCIHVDTSQCCPQCKERKNYCEFRGKTYQTLEEFVVSPCERCRCCEANGEVL
CTVSACPQTECVDPVYEPDQCCPICKNGPNCFAETAIVIPAGREVKTDECTICHCTYEETWR
IERQAMCTRHECRQM
```

Important features of the protein:

Signal peptide:

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

FIGURE 5

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTTGGGGTGCCAGGA
CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAAGCTGGTGTCTCCAAGGGTGCACGG
AGGCCAAGGACCAGGAGCCCGCTCACTGAGCACCGGATGGGCCCCGGCTCTCCCTGATC
TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACACACACTGTTATGAT
GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCAATCTGAGAGTCCAGGGATGCATGCC
CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
ACTGCAATAGGAAAGATTTTCTGACCTGTCTCGGGGGACCACCATTATGACACACGGAAC
TTGGCTCAAGAACCCACTGATTGGACCATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
GTGTGAGGAGCGCTGCTGCTCATAGATGTAGGACTCACATCAACCCTGGTGGGGACAAAAG
GCTGCAGCACTGTTGGGGCTCAAAATTCCAGAAGACCACCATCCACTCAGCCCTCCTGGG
GTGCTTGTGGCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
CAGCGTTCTGCTGAACCTCCCTCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTG
CTACCTGTGTGCAGCCCTTGGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
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CCCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCTTGGACACAGATTCTTTTC
CCATTCTGTCCATGAATCATCTTCCCAACACAATCATTATCTACTCACCTAACAGCA
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GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

FIGURE 10

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PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTHCYDGLRLRGGGIFSNLRVQGCMPQPGCN
LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
LLIDVGLTSTLVGTKGCSVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLCSASSSSVLLN
SLPPQAAPVPVGDRCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAQPSSFLLNHTRQIGIFSAREKRDVQPPASQHEGGGAEGLES�TWGVGLALAPALWWGVVCPSC
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 243-260

N-glycosylation sites.

amino acids 46-49, 189-192, 382-385

Glycosaminoglycan attachment sites.

amino acids 51-54, 359-362

N-myristoylation sites.

amino acids 54-59, 75-80, 141-146, 154-159, 168-173, 169-174,
198-203, 254-259, 261-266, 269-274, 284-289, 333-338, 347-352,
360-365, 361-366, 388-393, 408-413, 419-424

FIGURE 11

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCGCGCGCCCTG
GCTGCGCGCTGCTCTCGTGCCTTGGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGC
CTCGTGCCTCAGCCCTATTTCGGCACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTAT
TGTGCGGGCCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTG
CAGCTGGTCGCCCTCATTGCGCACGGCACCCGCTACCCACGCTCAACAGATCCGCAAGCT
GAGGCAGCTGCACGGTGTGTCAGGCCCGCGGGTCCAGGATGCGCGGGCTAGTAGTACCG
GCAGCCGCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGAC
GGGAGCTAGTAGAAGGACCGCAGGATATGCGACAGCTGGCGCTCGCTCTGGCCTCGCT
CTTCCCGGCCCTTTTCAGCGGTGAGAACTACGGCCGCTGCGGGTCAATCACCAGTTCCAAGC
ACCGCTGCATGGATAGCAGCGCCGCTTCTGTCAGGGGCTGTGGCAGCACTACCACCCTGGC
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TTTTATGAAGATCTGAAGAACCACTACAAGGACATCCTTCAGAGTTGTCAAACCAAGTGAAGA
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AAGTCAGATAGTTAGAATCGAAGTTTTCAAATCCATTGCTTAGCTAACTTTTCACTCTGT
CACTTGGCTTCGATTTTTATTTTTCTATTATATGAAATGTATCTTTTGGTGTGTTGATTT
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FIGURE 12

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RDLGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHR
CMDSSAAFLQGLWQHYPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYH
VEAFKTGPMEQNILKKVAATLQVPVNDLNADLIQVAFFTCSDLAIKGVKSPWCDVFDIDDA
KVLEYLNDLKQYWKRGYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAE
TLLPLLSLMGYFKDKPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRV
QMLLNEKVLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSEDEL
```

Important features:

Signal sequence

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

FIGURE 13

GGGACTACAAGCCGCGCCGCGCTGCGCCTTGGCCCCCTCAGCAACCCCTCGACATGGCGCTGAGGCGGCCACCCGCGAC
TCCGGCTCTGCGCTCGGCTGCGCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCTGATAGGGGCTGTAATCT
TCAAATTCAGCAATTCGAACCCCGATGGTACAGGAATTTGAAAGTGTGGAATCTGCTTGATCATTTACCGAATTCGC
AGACAAGTGACCCAGGATCTGAGTGGGAAGAAATTCAGATGAACAACACATATGTGTTTTGTTGCAACAACAAA
TTCAAGGAGACTTGGCGGCTGTCGAGAAATACTGGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTTATCGCTGTGAGGTGCTGTGCTCGAAATGACCGCAAGGAAATGATGAGATTTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCCGAAGGCTGTACCGATAGGCAAGATGCAACCACTGC
ATGCGCAGGAGAGTGAGGGCCACCCCGGCCCTCATTACAGCTGGTATCGCAATGATGTACCACTGCCCAACCAAT
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AGATGGAAGTCTATGACTGAACATTGGCGGAATTTATGGGGGGGTTCTGGTGTGCTTGTCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGCGACTTCAGACACAAGTCATCGTTTG
TGATCTGAGACCCCGGTTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAATCTCTGCTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTATTCAAGACTTTTCGTTTTGGCCAAAGTTGACCA
CTACTCTTCTACTCTAAACAAGCCACATGAATAGAGAATTTTCTCAAGATGGACCCCGGTAATATAACCAAA
GGAAGCGAAACTGGGTGGCTTCACTGAGTTGGGTTCTCTAACTGTGTTCTGGCCGTGATCCCGCATGAGATTAGG
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CAGCAGCCAGACAGCAACCATGTGAGAGTGGCGAGTGGCTGGACAGCCACAGCGCATCCCGGGCGCAACCA
GAAAAGGCTCTTACACAGCAGCCTTACTTCAATCGGCCACAGACACCACCGAGTTTCTCTTAAAGGCTCTGC
TGATCGGTGTGTCAGTCTCAATTTGTGGAGAAGCTTTTGGATCAGCAATTTGTAAAAACAACCAAAATCAGGAAG
GTAAATTTGGTGTGTCGGAAGAGGGATCTTGCTGAGGAACCTGCTTTGTCAACAGGGTGTGAGGATTTAAGGAAA
ACCTTCTGCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTTATTTTATAAAATTT
TACATCTAAATTTTGTCTAAGGATGATTTTGTGATTTAGAAAGAAATTTCTATTTAAACTGTAAATATATGT
CATACAAATGTTAAATTAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTCATAGTGTAAAT
TGGAAAAATATCAATAATTAAGATGATTTTACCAGGAATCTCTCATGGAAGTTTACTGTGATGTCTCTTTCT
CACACAAGTTTATAGCCTTTTTCACAAGGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTCAGTTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAATC
GCCTCTTCTGAGATGACTAGGACAGTCTGTACCAGAGGCCACCCAGAAGCCCTCAGATGTACATACACAGATG
CCAGTCAGCTCCTGGGTTTGGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCCTGCTGTCTGCAAGGAGGCCCT
GCCATCTTGGGCCCTGGCAGTGGCTGTGTCAGTGAAGCTTACTCAGTGGCCCTTGCTTCACTCCAGCAGC
TCTCAGGTGGGCATGCAAGGACACTGGTGTCTTCCATGTAGCGTCCAGCTTTGGGCTCCTGTACAGACCTCT
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTAAAGTTTGTTTAATTTATTTGT
AAGATTGCTCAAGGCAAAAGGCAATTCGAAATCAAGTCTGTCAAGTACAATAAATCTTTAAAAAGAAATGGAT
CCCATGTTCTCTTTGGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATCTCAAAACAAACCATGAT
GGAGTGGGCGCAGCTCAGCCTTTTAAAGAACGCTCAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGGAGGAAAG
TGAAGCGCCTGAATCAAAAGCAGTTTTCTAATTTTGACTTTAAATTTTCAATCGCCGGAGACACAGCTCTCCCAT
TGTGGGGGGAATCTAGCAACATCACTCAGAAAGGCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACTGCGCCCT
GCCGTGCTGGACTCAGGACTGAAGTGTCTGTAAGCAAGGAGCTGTGAGAAAGGAGCACTCCACTGTGTGCTGGA
GAATGCTCTCACTACTCACTTGCTTTTCAAGTCTCCAGTGTCTGGGTTTTTTATATCTTTGACGACTTTTTTT
AATTGCTACATACAGACTGTGTGACTTTTTTATGTTATGTGAAACCTTTGCGCAGGCGCCTGGCAGAGGCA
GGAATGCTCAGCAGTGGCTCAGTGTCCCTGGTGTGCTGCTGATGGCATCTGGATGCTTAGCATGCAAGTTCT
CTCTCCCTGGCACTCTGTAGAGAGGATGGCTCCCACTCAGCGTGGGAGTTCAAGCTCCAGCTCCAGCTCTCT
TCTTGGTTGTATAGTGATAGGTTAGCCTTATTGCCCTCTTCTTATACCTTAAACCTTCTACACTAGTGCCA
TCGGAACAGGCTCTGAAAGATAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGTGTCTTAATCTGAGACTAGA
CGAAAGGAATACTCGTGATTTTAAAGATAGAACTGCACTCAAGACTCGGCGGATACAGGCTGTGATCT
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CTCATTATAAAGCTTCAAAAAACCCA

FIGURE 14

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDNLNIGGIIG
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

FIGURE 15

CAGGACCAGGTCCTTCTACGCTGGAGCAGCGGGAGACAGCCACCATGACACATCTCTGGTCCATGCCATGGTG
 ATCTGCTGACGCTGGGGCCGCTCTGAGCCGACGACAGCGAGTTCAGGCGCTGCTGGACATCTGGTTTCCGGAG
 GAGGAAGCAGTGCCTCCGCTCTCTGGTGGACACATCGGAGGAGGCGCTGCTGCTCTCTGACTGGCTGAGCTG
 CGCATGATCCGTTCTGAGGTGCTCCGCTGGTGGACGCCGCTGACGAGCCTGGAGCCCGCAGCAGCTGCTGCTG
 TTCTGTCAGCTGTTTGGCATCCCCGTCTCAGCATGAGCAAACTCTCCAGTTCCTGGACCAGGCACTGCCCCAC
 GACCCCCAGACTCTGGAGCAGAACATCATGGACAAGAATTACATGGCCCCCTGGTGGAGGTCACGATGAGCGC
 GGGCGCTCCGAGGGCCAGACTTCCACTCTTGTCTACAGCCTCCCTGCGCCCCCCCGAGACAGCACAGAGGGA
 CCCAAACAAAGAGCAGCCAGACAGCCCATAGGCCAGGGCCGGATTGCGGTGGGGGACCCAGCTCCGGGTGCTG
 GGCCTTGAGGACGACTGGCTGGGATTCCTCCAGATTTCCTGCTCAGCGACCTGAGGCGGAGCCTCGGTGGCAGGCTCC
 AGTCCCGGCCCCGTGGCCCTCGCCCTGACAGAGGCCCTGGGGCAGGAGCTGGGCCCGGCTCGTCCAGGGCAGCCCC
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 GTGATGTCCATGCACCGTAGCCACTCTCTGGCTGCCCCGCTGCTGCGCCAGCTCTGCCAGTACACGCGCTGTGTG
 CCACAGGACACCGCTCTCTCTCGCTCTTCTGAAAGGTGCTCTGACAGTGTGCACTGGCTGGACAGCCCTGGC
 GTGGAGGGCGGGCCCCCTGCGGCACAGCTCAGGATGCTTGCACGACAGCCCTCAGCGGGCGAGGCTCAGTGAT
 GTGCGAGGGGGCTCTCTGCGCTGCGCCAGGCCCCCTGGCCTTCCTGACGAGCTGGAGGTGTGACGTCCACCGCT
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 GGGCTGATCGAGGTGAGGTCTCCCCACTGGAGGAGCTGCTGACTGCTATTCTCTGCCACTGGGATGCTGCC
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 GGGAGAGCCGGGTGCGGACGGTGGAGGCGCTGGGCGCTGCGCTGCGGACCTCTGTCAGGCTCTCATGTGGACTG
 CTGGAAATGCTGGAACCCGAGGTGCTCAGCAGCTGCCCGACCTGACGCTCAGGCTGCTCTTCTCCGGAGGCTG
 GGCAAAGGTGAGGCCAGGTGCCCCCTGCTTCCGCTCCCTACCTCTGACCCCTTTCACGACATCAGTCCAGCTGGCCCC
 ACCTGCAACAGTGCATCCGAGTCTGCTGGGCAAGAGCCGGGAACAGAGGTTCCAGCCCCCTCTGCTCTCTGGAC
 TTCTCTGGGCTGCATCCATGTTCTCTGCTATCTGGCAGGGGCGGGACAGCGCACCCCGCAGAAAGCGCGGGAG
 GAGCTGGTGTGCGGGTCCAGGGCCCGGAGCTCATAGCCTGTGTGGAGCTGATCTTCCGCGAGGCGGAGACGCG
 AGCCAGGACGGGACACAGCCGCTGACGCTCATCAGGCCCGGCTGCCCTGCTGCTCAGCTGCTGCTGTGGG
 GACGATGAGAGTGTGAGGAAGGTGACGGAGCACCTGTACGGCTGATCATCAGCAGTGGGAGACAGCGTGTGGGA
 AGCGCTGCGGAGACCTTCTCTGACGCTCTACCTACAGCGCCCGGAGCTGGGGGTGCCCGTCTGCTAGGTTCTTA
 CTGCAACAGGAAGGGCTGCCAGCAGCAGCTGTCGAAAGTGGACGGACTCATCCACCCTTCATCAGCTCCTT
 GCGGACACCAAGCACTCCCGGCGTTGGAGAACCAGAGGGGCGATGCCAGCATGGCTTCCGCGGAAGTCTGGCGTG
 GCGCACCCGCTGCTGCTGCTCAGGCACTGCCATGATCGCGCGCTCTGCAAGCGCGCACCCACCTCAACTTC
 CAGGAGTTCCCGCAGCAGAACCACTGAGCTGCTTCTGCAAGTGTCTGGGCTGCTGGAGCTGCTGACCCGCGAC
 GTGTCCCGCAGCAGCACAGGGGGCGCTGGGACTGCTTCTGCTCTCATCCGCTGCTGCTGCTGAATTACAGG
 AAGTCTCCCGCATCTGGCTGCTTTCATCAACAAAGTTTGTGCAGTTTCATCCATAAGTACATTACATAATGCC
 CCAGCAGCATCTCTTCTGCAAGACAGCGCCAGCCGCTCCACGACCTGTCTTTCAGAACAGTGACCTGGTG
 ATGCTGAAATCCCTCTTTCAGGGCTCAGCTTGCCAGCAGGAGGACGACGAGCAGCAGGACGAGGCTGGAGGAAG
 GGGCAGGAGAGAGCTCAGCCGCTCTTGCCTGTGTCAGCTCTCTCCCTGACCCCTCTGACCCGCGCCGAG
 ATGGCCCCCTACATGAACCGGCTTTCGCGGGCCAAACGCTGGAGGATCTGCTGGAGGTTCTGAGTGACATAGAC
 GAGATGTTCCCGCGGAGACCCGAGACTCTGAGCTTCTTCGACCAACCTGACGCGGCTGATGAGCTCGGCCGAG
 GAGTGTGTCGCGAACCTTCGCTTCAGCCTGGCCCTGCGCTCCATGCAGAACAGCCCCAGCATTGACGCGCTTTC
 CTGCCCCCTGTATGATAGCTGCTGGGCAGCCAGGACTTTGAGGTGGTGCAGCGGCCCTCCGGAACCTGCCTGAG
 TACGCTCTCTGTCGCAAGAGCAGCGGCTGTGCTGCTCCACCGGCTCTCTGTTGGGCGATGTACGGCCGAGT
 GACCCAGCGCGCAGATCTCCAGGCCCTGAGGATCTGTCATATGAGGGCGGTGATGTGAGCCTGTGGCAGCCGA
 CCCCCCTCAGGCCCGCCGCTGCTGCTCCCGGGATCTCTCGAGCAAGCCAGGAAGCTGGGCGTGGGCTGCTG
 TCTGTCCGAGGAGTGAAGGCGCCGAGCCCTGAGGCCAGGACAGGCCAATACCTCCGAGCCCTGGGCTGG
 CTCGCGGCGGCGGCTGCGCATCAGGGGCCGCTCCAGCAGCCCTCATTCACCTCTGGGCGCAGCCCTGCCGCGG
 AGCGGGATCCCCCGGACATGCTGGGCTGGTTTGAATGAACGACCTGACTGCTCA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77631

><subunit 1 of 1, 1029 aa, 1 stop

><MW: 114213, pI: 6.42, NX(S/T): 0

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MAHLVEVQHERGASGGQTFHSLLTASLPRRDSTEAPKPKSSPEQPIQGGRIRVGTQLRLVLG
PEDDLAGMFLQIFPLSPDPRWQSSSPRPVALALQQALGQELARVVQGSPEVPGITVRVLQAL
ATLLSSPHGGALVMSMHRSHFLACPLLRLQCQYQRCVPQDTGFSSSLFLKVLLQMLQWLDSFG
VEGGPLRAQLRMLASQASAGRRLSDVRGGLRLAEALAFQDLEVVSSTVRAVIATLRSGEQ
CSVEPDLLISKVLQGLIEVRSPHLEELLTAFFSATADAASFPACKPVVVVSSLLQEEEP
GGKPGADGGSLEAVRLGPSSGLLDVWLEMLDPEVVSSCPDLQLRLLFSRRKGKGQAQVPSFR
PYLLTLFTHQSSWPTLHQCIRVLLGKSREQRFPDPSASLDPLWACIHVPRIWQGRDQRTPOKR
REELVLRVQGPPELISLVELILAEATRSQDGDTAACSLIQARLPLLLSCCCGDDESVRKVTE
HLSGCIQWGDSDVLGRRCRDLLLQLYLQRPRLRVVPVEVLLHSEGAASSVCKLDGLIHRFI
TLADTSDSRALENRGADASMACRKLAVAHPLLLRHLPMAIALHGRTHLNFQEFRRQNNHL
SCFLHVLGLLELLQPHVFRSEHQGALWDCLLSFIRLLNRYKSSRHAAAFINKFVQFIHKYI
TYNAPAAISFLQKHADPLHDLSDNSDLVMLKSLLAGLSLPSRDRDTRGLEDGEEGEESAG
SLPLVSVSLFTPLTAAEMAPYMKRLSRGQTVEDLLEVLSDIDEMSRRRPEILSFFSTNLQRL
MSSAECCRNLAFLSLRLSRMNSPSIAAFLPTFMYCLGSQDFEVVQTALRNLPYALLCQE
HAAVLLHRAFLVGMYGQMDPSAQISEALRILHMEAVM

Important features:

Signal peptide:

amino acids 1-16

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 154-158, 331-335, 616-620, 785-789, 891-895

N-myristoylation sites.

amino acids 91-97, 136-142, 224-230, 435-441, 439-445, 443-449,
665-671, 698-704

Amidation sites.

amino acids 329-333, 634-638

[illegible]

CCGGGCCATG CAGCCTCGGCCCGCGGGCGCCCGCGCGCACCCGAGGAGATGAGGCTCCGG
AATGGACCTTCTGTGACGCTGTCTCTTCTGCTCTGTGCGCTTCTCTCTGCTGTCTGGTA
CGCGGCATCTCAGCGCCGAGAAGCGACGTTGTGGACGTTTACACGCGGAGGATTCCTGGCGC
TGCGCGATCGGTTG CACG CAGCTGAGCAGGAGAGCCTCAAGCGCTCCAAGGAGCTCAACCTG
GTGCTGGACGAGATCAAGAGGCGCGTGTCAAGAAGGCAGCGCTCGCAGACCGGAGCGGCAA
TCGCACCTGGGCGCGCTTAACAGAGACCCTCCGTTGAAGCGCTGGAACGGCTCACCCGAC
ACGTGCTGCACCTGCCACCGTCTTCCATCACCTGCCACCTGCTGGCCAAGGAGAGCAGT
CTGCAGCCGCGCGTGC GCGTGGGCGAGGCGCGCACCGGAGTGTCCGTGGTGATGGGCATCCC
GAGCGTGGCGCGAGGTGCACCTGCTACCTGACTGCACTTGACTCGCTCATCTCCGAGC
TGAGCCCGCAGGAGAAGGAGACTCGGTATCGTGGTGCTGATCGCGGAGACTGACTCACAG
TACACTTCGGCAGTGACAGAGAACTCAAGGCGCTTGTTC CACGAGGAGTCCATTGTGGGT
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TTGGGAGCCCAAGGAGAGTCAAGTGGAGGACCAACAGAACCTCGATTACTGCTTCTCT
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GCCCAACTACTTGAGCACCATGAAGAAGACTTGACATGTCAGCAGCCTTACAGAGGACTGGATGA
TCTTGAGTCTCCAGCTGGGCTTCATTGTTAAGTGTTC AAGTCGCTGGACCTGGAGCGTG
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TCTGTGGGTGAAAGTCTGCAACCCGAGGAAGGTGCGAAGCATGTGACCGGCGAAGAGCCT
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GGCAAGATCCAGAAACTGAAGGACAAAGACTTTGGAAGCAGGCGCTGCGGAAGGAGCATGT
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CCTACCTCGCGAGGACTTCTTCTGGGCTTCAACCTCGCGGGGACTCTATCCGCTTC
CGTCTCTTCAACCTCTAAGACTGGAGCGTCTTCTTCCGAGTGGGAACATCAGACACC
GGAGGACAAGCTCTTCAAACGCTCTGTGAGGTTGCTGCCCTTCGACAACCTCAGTCAGACA
AGGAGGCCCTCGAGGAGGCGCAGCCGCACTTCCGGTACCTCGGAGCCCCGACGCTA
CTCCAGATCGGCTCTCTTACAAAGGAGTGCAGAGGAGAGTGAACCGAGCTCTCGGCC
TCTGGAAGCACTGCGCCTCTCGATCCAGACGCACTCCCTGTGTGGGTGATTCTGAGCGAGA
TCTTCTGAAAAAGGCGCAGTAAAGCTGCGGCTCTGAGGGTCACTGTGGCGAGCCCTGAA
GCCCATTTCTTGGGGTGCTGTCACGTGCGCTCCCGAGGAGGCGAGATACGCGCCCGCCAAA
AGGGCTTCTGCTGGCGTGGGCTTGGGCGGCGCTGGGGTCCGCGCTGGCCCCGAGGCCCTA
GGAGCTGTGTGCTCGCCCCGCCCCGCGGCGGAGGAGGAGGAGGCGCGCCCCCACTGTGCC
TGAGGCCCGGACCGTTGCAACCCGCGCTGCCCACTCAGGCTAGCTCTTTAGAAGAGCTTTTAT
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AAAAAAAAAAAAAAAAAAAA

FIGURE 18

```
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KESSLQPAVRVGQGRGTGVSVVMGIPSVRREVHSYLTDTLHSLISELSPOEKEDSVIVVLIAE
TDSQYTSAVTENIKALFPTEIHSGLLEVISPSPHFYDPDFSRLRESFGDPKERVVRWRTKQNL
YCFLLMYAQSKGIYYVQLEDDIVAKPNYLSTMKNFALQQPSSEWMILEFSQLGFICKMFKSL
DLSLIVEFILMFYRDKPIDWLLDHILWVKVCNPEKDAKHCDRQKANLRIRFKPSLFQHVGT
SSLAGKIQKLKDKDFGQALRKEHVNPPAEVSTSLKTYQHFTLEKAYLREDFFWAFTPAAGD
FIRFRFFQPLRLERFFFRSGNIEHPEDKLFNTSVEVLPFDNPFQSDKEALQEGRTATLRYPRS
PDGYLQIGSFYKGVAEGEVDPAFGPLEALRLSIQTSPVWVILSEIFLKKAD
```

Important features:

Signal sequence

amino acids 1-23

N-glycosylation sites.

amino acids 5-9, 87-91, 103-107, 465-469

N-myristoylation sites.

amino acids 6-12, 136-142, 370-376, 509-515